

II. NATIONAL WHEAT GENOMICS CONFERENCE
**2008 National Wheat
Genomics Conference**

**1–2 December, 2008.
Indianapolis, IN, USA.**

Update on the NWIC Subcommittee on Wheat Genomics.

Eduard Akhunov was elected as the new university representative. The current subcommittee membership is listed in the table below. Please do not hesitate to contact any of us on issues that you think will be important for the subcommittee to discuss. Information about the committee can be found at: <http://wheat.pw.usda.gov/NWIC/>

Role (term duration)	Name	E-mail
Chair (2009)	Stephen Baenziger	Pbaenziger1@unl.edu
NWIC Representative (2009)	Jim Anderson	ander319@umn.edu
Industry/Nonprofit Representative (2010)	Rollie Sears	rollin.sears@syngenta.com
Industry/Nonprofit Representative (2011)	Jay Romsa	jay.romsa@genmills.com
University Representative (2011)	Eduard Akhunov	eakhunov@ksu.edu
University Representative (2010)	Mark Sorrells	mes12@cornell.edu
USDA Representative (2010)	Olin Anderson	oanderson@pw.usda.gov
USDA Representative (2011)	Justin Faris	justin.faris@ars.usda.gov
At-large Representative (2009)	Ed Souza	souza.6@osu.edu
IWGSC (ex officio)	Kellye Eversole	eversole@eversoleassociates.com

The subcommittee will meet annually, but the next meeting of the whole community will be every other year beginning in 2010. **Mark your calendars:** A Joint Congress, combining the Hard Winter Wheat Workers Regional Workshop and The National Wheat Genomics Workshop, will be held 7–10 March, 2010, at the Embassy Suites, Lincoln, NE.

Finally, the summarized results of the second national survey of genomics priorities for wheat which was undertaken by The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics. The full survey results are attached below and can be found at: <http://wheat.pw.usda.gov/NWIC/WheatResPrioritiesSum08F.pdf>.

The survey was distributed at the second annual National Wheat Genomics Conference (approximately 65 researchers attended) and by a directed e-mail solicitation so that those unable to attend the meeting could share their views and have input. Every effort was made to insure the survey was widely distributed among the U.S. wheat research community. At the annual meeting, the main theme was wheat genomics and aspects of wheat research related to genomics. Briefly summarized the research priorities are to

- 1) expand molecular mapping of economically important traits,
- 2) increase molecular marker development to better cover the wheat genome,
- 3) develop a physical map of the hexaploid wheat genome,
- 4) improve ease-of-use and interoperability of wheat-related databases, and
- 5) exploit functional genomics to understand gene expression and gene networks.

If you have any questions concerning the survey, please do not hesitate to ask. Also please share this survey with whomever you think would appreciate knowing these results. The results of the survey have also been included in The 'NWIC/NAWG Research Priorities for FY10' booklet, which is posted at <http://cropandsoil.oregonstate.edu/wheat/reports/NWIC/index.htm>.

In the NWIC/NAWG Research Priorities for FY10, they state 'The NWIC and NAWG support the goal of advancing wheat genomics to serve as the foundation for basic research and provide the tools for improving food, fuel, and crop yields in a changing environment. We support increased funding of these efforts through collaborative national research grants, such as those sponsored by USDA–NIFA Agriculture and Food Research Initiative and the National Science Foundation.'

In 2006, the NWIC authorized the formation of a Subcommittee for Wheat Genomics, comprised of seven elected members, representing university and USDA–ARS researchers, industry, and nonprofit agencies. The goal of the Subcommittee for Wheat Genomics is to facilitate communication among U.S. researchers, assess national genomics research needs and goals, develop strategies and organize research efforts, facilitate communication with national granting agencies and participation in international initiatives, and advocate for funding of wheat genomics research at the national level.

Guiding principles.

- Wheat is the ideal model species for studying polyploid genome evolution and trait variation because of the unmatched complement of aneuploid genetics stocks, natural diversity, and wide adaptation.
- Public wheat breeding and research is critical to U.S. agriculture because three quarters of all wheat cultivars were developed by public wheat breeders.
- The open exchange and publication of wheat research contributes to the rapid advancement of new scientific knowledge for improvement of wheat and other crops.
- The study of polyploidy genetics and gene expression will provide key information about how genes and alleles interact in a polyploid genome.
- Wheat research has led to novel discoveries in the genetics and biology of vernalization, genetic control of chromosome behavior, and end-product quality.
- Wheat cytogenetics has made major contributions and continues to provide novel genetics stocks and other tools for understanding mechanisms of chromosome pairing and for chromosome manipulation.'

National Wheat Improvement Committee Subcommittee on Wheat Genomics.

4–6 December, 2008.

Indianapolis, IN, USA.

Executive Summary – The future of wheat genomics research in the United States. The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics held their second annual meeting, The National Wheat Genomics Conference (NWGC). The purposes of the meeting were to provide a venue for U.S. wheat workers to learn of current endeavors in U.S. wheat genomics and related research and to provide a forum to foster interaction, discussion, and collaboration among wheat scientists. The meeting also provided the opportunity to formulate and communicate the future research needs of the U.S. wheat-genomics community. Although the main theme of the conference was wheat genomics, the session topics and presentations encompassed other aspects of wheat research related to genomics. To guide strategic planning, key speakers relating to critical research topics important for the future of wheat improvement were invited to give presentations. These research topics were considered relative to the overarching goal of understanding the genetic basis of traits in wheat. The research topics listed below, and the prioritized research necessary to achieve the goal of advancing wheat genomics, serve as the foundation for basic research and provide the tools for improving food, fuel, and crop yields in a changing environment. Based on surveys distributed at the conference and a directed e-mail solicitation, the **top five wheat genomics research priorities are**

- 1) increased support for mapping traits of economic importance for molecular breeding,
- 2) more molecular markers,
- 3) a physical map of hexaploid wheat genome,
- 4) improved ease of use and interoperability of wheat-related databases, and
- 5) to study functional genomics to understand gene expression and gene networks.

Recently funded projects that were listed in past surveys. Complete, anchored physical map of *Ae. tauschii* (highest priority in 2007) and wheat radiation hybrid mapping to initiate genome sequencing.

Key research topics that define our research goals and priorities.

- Wheat is the ideal model species for studying polyploidy genome evolution and trait variation because of the unmatched complement of aneuploid genetics stocks, natural diversity, and wide adaptation.
- Public wheat breeding and research is critical to U.S. agriculture because three quarters of all wheat varieties were developed by public wheat breeders.
- The open exchange and publication of wheat research contributes to the rapid advancement of new scientific knowledge for improvement of wheat and other crops.
- The study of polyploidy genetics and gene expression will provide key information about how genes and alleles interact in a polyploid genome.
- Wheat research has led to novel discoveries in the genetics and biology of vernalization, genetic control of chromosome behavior, and end-product quality.
- Wheat is well situated to continue as a leading model for comparative genomics and genome evolution.
- Wheat cytogenetics has made major contributions and continues to provide novel genetics stocks and other tools for understanding mechanisms of chromosome pairing and for chromosome manipulation.

Community resources will help achieve our research goals. To advance these research areas, community resources must be created or strengthened. The questionnaire below was distributed to attendees of the Wheat Genomics Conference and also sent to U.S. wheat researchers by e-mail to develop a consensus of priorities among wheat researchers in the U.S.

Prioritize general community needs (1 = highest rank; rank up to five topics).

- _____ Centralized catalog of genomics resources available to the community
- _____ Increased support for mapping traits of economic importance for molecular breeding
- _____ Improved doubled haploid technology
- _____ Enhanced quantitative genetics methods and tools
- _____ Improved ease of use and interoperability of wheat-related databases
- _____ Complete genome sequence of *Aegilops tauschii*
- _____ Physical map of hexaploid wheat genome
- _____ Genome sequence of hexaploid wheat gene space, potentially linked to the genetic map
- _____ Draft BAC sequences for the entire hexaploid wheat genome
- _____ Full-length wheat cDNA collection (sequences and clone access)
- _____ Functional genomics studies to understand gene expression and gene networks
- _____ More molecular marker development including SNPs and SSRs
- _____ Improved wheat transformation methods
- _____ TILLING populations and services for different classes of wheat
- _____ A second BAC library for hexaploid wheat genome
- _____ Other _____

Response to questionnaire. Forty-one responses were received. The rank is based on the number of scores a topic received (count) as well as the average score. The index was calculated as 'count /average score', thus, the index reflects both average score and the number of times the topic was selected as a priority. Topics are shown in the original order that they appeared on the survey.

Rank	Count	Average	Index	Topic
11	10	2.9	3.4	Centralized catalog of genomics resources available to the community
1	27	2.2	12.2	Increased support for mapping traits of economic importance for molecular breeding
8	13	3.4	3.8	Improved doubled-haploid technology
13	10	3.4	2.9	Enhanced quantitative genetics methods and tools
4	18	2.8	6.5	Improved ease of use and interoperability of wheat-related databases
6	14	2.7	5.2	Complete genome sequence of <i>Aegilops tauschii</i>

Rank	Count	Average	Index	Topic
3	17	2.1	8.0	Physical map of hexaploid wheat genome
9	13	3.4	3.8	Genome sequence of hexaploid wheat gene space, potentially linked to the genetic map
14	5	4.2	1.2	Draft BAC sequences for the entire hexaploid wheat genome
7	14	3.4	4.2	Full-length wheat cDNA collection (sequences and clone access)
5	18	3.2	5.7	Functional genomics studies to understand gene expression and gene networks
2	22	2.6	8.5	More molecular marker development including SNPs and SSRs
10	14	3.7	3.8	Improved wheat transformation methods
12	12	4.0	3.0	TILLING populations and services for different classes of wheat

Other Topics written on the surveys.

- 3 – A second BAC library for hexaploid wheat genome
- 5 – Need for a regional, perhaps USDA operated facilities for production of doubled haploids and transformation
- 1 – Wheat small-RNA targeting libraries
- 1 – Improved markers for end-use quality traits
- 2 – VIGS, transformation, and RNAi-related research
- 3 – Bioinformatics tools so breeders can properly integrate marker information in a molecular breeding strategy

Assessment of 2008 survey results. The results of this survey differed substantially from the 2007 survey. The highest priority was for a new topic that was suggested in the ‘Other’ category in last year’s survey. That topic was ‘Increased support for mapping traits of economic importance for molecular breeding’, which was likely influenced by the Wheat CAP project which is ending in 2009. ‘More molecular marker development’ moved up to second and ‘Physical map of hexaploid wheat genome’ dropped to third. ‘Improved ease of use and interoperability of wheat-related databases’ remained in fourth place. ‘Functional genomics studies to understand gene expression and gene networks’ was ranked fifth, whereas the fifth topic last year, ‘Full-length wheat cDNA collection’, dropped to seventh.

Wheat researchers who responded to this year’s surveys placed a high priority on the use of molecular markers for mapping economic traits in wheat and new marker development is essential for that activity. Wheat genomics researchers also recognize the value of physical maps. A physical map for *Ae. tauschii* was the highest priority last year, and it was funded by NSF. A physical map of hexaploid wheat was second last year and third this year. Wheat-related databases have ranked high in all of our surveys, because they are recognized as an essential tool for all wheat research. The lowest ranking topics were quite different from last year. Last year, the three lowest priority topics were si(micro) RNA collection, improved coordination of RFPs from NSF and the USDA, and improved wheat-transformation methods. This year, the three lowest priority topics were draft BAC sequences for the hexaploid wheat genome, enhanced quantitative genetics methods, and TILLING populations and services. Five respondents wrote in ‘Facilities for production of doubled haploids and transformation. Of the 14 topics, sequencing priorities ranked 6, 7, and 9, almost identical to 2007. These results reflect a very strong and pressing need for marker resources, online databases, and physical maps relating to positional cloning, mapping traits, and marker-assisted selection as compared to genome sequencing, transformation, and TILLING population research. The success of the Wheat CAP project has clearly had an impact on the priority topics in this survey compared to 2007.